

SEQUENCE LISTING

<110> LUKYANOV, Sergei Anatolievich
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 YANUSHEVICH, Yury Grigorievich

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA
 SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<141> 2005-04-26

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

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gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc	240
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gatcacaggg ataacatgag cttgggtgaa accgtacggg ctgtggattg cagaaaaaca	720
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<210> 2

<211> 234

<212> PRT

<213> Phialidium sp.

<400> 2

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 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95
 Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 3

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

<400> 3

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gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat 240
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<210> 4

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20           25           30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35           40           45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50           55           60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65           70           75           80
Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
          85           90           95
Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
          100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
          115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
          130          135          140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160
Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe

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gtcaaactta	atggacaagg	atttaagaaa	gacggacatg	tgcttggaaa	gaatcttgaa	420
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tctgctttca	aaattcgcca	tgagattact	ggatcaaaaag	gagacttcac	tgttgcagac	540
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atgagctacc	atgtcaagct	cagcaaagat	gttactgac	acagggataa	catgagcttg	660
aaggaaaccg	tacgggctgt	ggattgcaga	aaaacatatc	tttaa		705

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30
 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 7

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 7

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cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660
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<210> 8

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 8

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20          25          30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35          40          45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50          55          60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65          70          75          80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
          85          90          95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
          100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
          115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
          130          135          140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
          165          170          175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro

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	180		185		190
Val	His	Val	Pro	Glu	Tyr
		His	His	Met	Ser
				Tyr	His
				Val	Lys
				Leu	Ser
	195		200		205
Lys	Asp	Val	Thr	Asp	His
		Arg	Asp	Asn	Met
				Ser	Leu
				Lys	Glu
				Thr	Val
	210		215		220
Arg	Ala	Val	Asp	Cys	Arg
		Lys	Thr	Tyr	Leu
225			230		

<210> 9
 <211> 705
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> humanized version of the phiYFP-M1
 <400> 9

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gtgaccaccc	tgacctacgg	cgcccagtgc	ttcgccaagt	acggccccga	gctgaaggat	240
ttctacaaga	gctgcatgcc	cgatggctac	gtgcaggagc	gcaccatcac	cttcgagggc	300
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agcgccttca	agatctgcca	cgagatcacc	ggcagcaagg	gcgatttcat	cgtggccgat	540
cacacccaga	tgaatacccc	catcggcggc	ggccccgtgc	acgtgcccga	gtaccaccac	600
atgagctacc	acgtgaagct	gagcaaggat	gtgaccgatc	accgcgataa	tatgagcctg	660
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<210> 10
 <211> 234
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> humanized version of the phiYFP-M1
 <400> 10

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Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
				20				25					30		

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 11

<211> 1047

<212> DNA

<213> hydromedusa 1 from sub-order Anthomedusae

<400> 11

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 ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaaccctg catacttggt 180
 gcaatgacag aacattttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240
 gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgtaatt 300
 gaaggaaaa atgtttgtac agaaggagaa gttcctatct catgggtttc gctcatcacc 360
 tcattaagtt atggtgcgaa atgttttggt cgatatccaa atgaaataaa tgattttttc 420


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gtgaaaggca caggcttcga taaagatggg catgtatgcc aaaaaaatct tgaatcctcc 600
cctccttcga caacatatgt tgttcccagag ggagaaggta ttcgaatcat ctatagaaac 660
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<210> 12

<211> 262

<212> PRT

<213> hydromedusa 1 from sub-order Anthomedusae

<400> 12

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          20           25           30
Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
          35           40           45
Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
          50           55           60
Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65           70           75           80
Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
          85           90           95
Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
          100          105          110
Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
          115          120          125
Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
          130          135          140
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145          150          155          160
Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
          165          170          175
Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile

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	180		185		190
Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala					
195		200		205	
Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala					
210		215		220	
Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp					
225		230		235	240
Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala					
	245		250		255
Phe Asp Ala Asp Phe Ser					
260					

<210> 13

<211> 1089

<212> DNA

<213> hydromedusa 2 from sub-order Anthomedusae

<400> 13

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtgggtg aatgatcaga      180
aattcacgat aatcgcagat ggatcgtcca aattccccc tggtgacttc aacgtgcatg      240
ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaat      300
acgggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgtc      360
ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt      420
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<210> 14

<211> 232

<212> PRT

<213> hydromedusa 2 from sub-order Anthomedusae

<400> 14

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Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
           20           25           30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
           35           40           45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
           50           55           60
Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65           70           75           80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
           85           90           95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
           100          105          110
Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
           115          120          125
Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
           130          135          140
Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145          150          155          160
Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
           165          170          175
Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
           180          185          190
Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
           195          200          205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
           210          215          220
Val Pro Arg Ile Thr Ser Ala Ile
225          230

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<210> 15

<211> 699

<212> DNA

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP

<400> 15

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gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaaccatt      180
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gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg      360
ataaccgtta attgtgacgg atttcaacct gatggacca tcatgagaga ccagcttggt      420
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atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata      600
accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc      660
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<210> 16

<211> 232

<212> PRT

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP

<400> 16

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Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
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          20           25           30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
          35           40           45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
          50           55           60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65           70           75           80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
          85           90           95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
          100          105          110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
          115          120          125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
          130          135          140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu

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145	150	155	160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His			
	165	170	175
Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro			
	180	185	190
Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser			
	195	200	205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser			
	210	215	220
Val Pro Arg Ile Thr Ser Ala Ile			
225	230		

<210> 17

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1

<400> 17

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atgtccagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc      60
aatgtgggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc      120
aagggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg      180
gtgaccaccc tgtcctacgg cgcccagtg ttcgccaaagt acggccccga gctgaaggat      240
ttctacaaga gctgcatgcc cgatgggtac gtgcaggagc gcaccatcac cttcgagggc      300
gatggcaatt tcaagaccgg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc      360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag      420
ttcaatttca cccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag      480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat      540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac      600
atgagcacc cgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg      660
aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga                          705

```

<210> 18

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
 225 230

<210> 19

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 19

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atgtccagcg gcgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc    60
aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc    120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcacctg    180
gtgaccaccc tgtcctgggg cgcccagtgc ttcgccaagt acggccccga gctgaaggat    240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc    300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc    360
gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag    420
ttcaatttca cccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag    480
agcgcttca agatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat    540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac    600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg    660
aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga                      705

```

<210> 20

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 20

```

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1           5           10          15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20          25          30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35          40          45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50          55          60
Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65          70          75          80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
          85          90          95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
          100         105         110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
          115         120         125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr

```

130	135	140
Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys		
145	150	155
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe		160
	165	170
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro		175
	180	185
Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser		190
	195	200
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu		205
	210	215
Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu		220
225	230	

<210> 21
 <211> 699
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> humanized version of the S3-2 mutant
 <400> 21

atggagggcg gccccgcct gttccagagc gacatgacct tcaaaatctt catcgacggc	60
gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc	120
gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc	180
tgccacctga tccagtacgg cgagcccttc ttcgcccgtc accccaacgg catcagccac	240
ttcgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac	300
gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgctg ggtgagccgc	360
atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg	420
gacatcctgc ccaacgagac ccacatgttc cccacaggcc ccaacgccgt gcgccagctg	480
gccttcatcg gcttcaccac cgccgacggc ggcctgatga tgagccactt cgacagcaag	540
atgaccttca acggcagccg cgccatcaag atccccggcc ccacttcgt gaccaccatc	600
accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc	660
tacgcccaca gcgtgccccg catcaccagc gccatctga	699

<210> 22
 <211> 232
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> humanized S3-2 mutant

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
 1 5 10 15
 Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
 20 25 30
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
 35 40 45
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
 50 55 60
 Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
 65 70 75 80
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
 85 90 95
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
 100 105 110
 Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
 115 120 125
 Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
 130 135 140
 Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
 145 150 155 160
 Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
 165 170 175
 Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
 180 185 190
 Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
 195 200 205
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
 210 215 220
 Val Pro Arg Ile Thr Ser Ala Ile
 225 230